

## SEQUENCE LISTING

<110> Presnell, Scott R.  
Kuestner, Rolf E.  
Gao, Zeren

<120> Human Cytokine Receptor

<130> 00-49

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)...(2344)

<400> 1

```

ccgccgcggc caccgcccac tcggggctgg ccagcggcgg gcggccgggg cgcagagaac   60
ggcctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc   112
                               Met Ala Pro Trp Leu Gln Leu Cys Ser
                               1               5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg   160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
  10              15              20              25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg   208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
          30              35              40

agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga   256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly
          45              50              55

gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa   304

```

Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys	
60 65 70	
tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att	352
Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile	
75 80 85	
gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa	400
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln	
90 95 100 105	
gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc	448
Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe	
110 115 120	
ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga	496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg	
125 130 135	
cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc	544
Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	
140 145 150	
ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt	592
Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe	
155 160 165	
gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac	640
Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn	
170 175 180 185	
gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg	688
Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu	
190 195 200	
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg	736
Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg	
205 210 215	
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac	784
Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp	
220 225 230	

cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag	832
His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys	
235 240 245	
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa	880
Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln	
250 255 260 265	
act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat	928
Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp	
270 275 280	
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg	976
Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met	
285 290 295	
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga	1024
His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg	
300 305 310	
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg	1072
Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr	
315 320 325	
ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca	1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser	
330 335 340 345	
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc	1168
His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu	
350 355 360	
cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc	1216
Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser	
365 370 375	
agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac	1264
Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr	
380 385 390	
ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa	1312
Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu	
395 400 405	

gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag	1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys	
410 415 420 425	
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag	1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys	
430 435 440	
tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc	1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly	
445 450 455	
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa	1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu	
460 465 470	
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt	1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe	
475 480 485	
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc	1600
Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile	
490 495 500 505	
cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc	1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu	
510 515 520	
tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag	1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln	
525 530 535	
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc	1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly	
540 545 550	
cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag	1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu	
555 560 565	
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca	1840

Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro	
570 575 580 585	
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt	1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val	
590 595 600	
tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta	1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu	
605 610 615	
aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag	1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln	
620 625 630	
cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct	2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro	
635 640 645	
gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa	2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys	
650 655 660 665	
gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg	2128
Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser	
670 675 680	
tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg	2176
Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser	
685 690 695	
acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct	2224
Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser	
700 705 710	
tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc	2272
Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu	
715 720 725	
tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat	2320
Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp	
730 735 740 745	

gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta agcattgccca 2374  
 Glu Leu His Ala Val Ala Pro Leu

750

ctttagctg 2383

<210> 2

<211> 753

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala  
 1 5 10 15  
 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg  
 20 25 30  
 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg  
 35 40 45  
 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn  
 50 55 60  
 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr  
 65 70 75 80  
 Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr  
 85 90 95  
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp  
 100 105 110  
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile  
 115 120 125  
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu  
 130 135 140  
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu  
 145 150 155 160  
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys  
 165 170 175  
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe  
 180 185 190  
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu  
 195 200 205  
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His  
 210 215 220  
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly  
 225 230 235 240

Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe  
 245 250 255  
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr Ser Cys  
 260 265 270  
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp  
 275 280 285  
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val  
 290 295 300  
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro  
 305 310 315 320  
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg  
 325 330 335  
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser  
 340 345 350  
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro  
 355 360 365  
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His  
 370 375 380  
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly  
 385 390 395 400  
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu  
 405 410 415  
 Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile  
 420 425 430  
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn  
 435 440 445  
 Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe  
 450 455 460  
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln  
 465 470 475 480  
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr  
 485 490 495  
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr  
 500 505 510  
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg  
 515 520 525  
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg  
 530 535 540  
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile  
 545 550 555 560  
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys  
 565 570 575

Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val  
 580 585 590  
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys  
 595 600 605  
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu  
 610 615 620  
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly  
 625 630 635 640  
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala  
 645 650 655  
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met  
 660 665 670  
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu  
 675 680 685  
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser  
 690 695 700  
 Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu  
 705 710 715 720  
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala  
 725 730 735  
 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala Pro  
 740 745 750  
 Leu

<210> 3

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc\_feature

<222> (1)...(2259)

<223> n = A,T,C or G

<400> 3

atggcncnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn	60
wsncarytng cngtngcngc ngnggnwnsn gngmngncnm gngngcnga yacntgyggn	120
tggmgnatga argcngcngc nmgnccnmgn ytntgygtng cnaaygargg ngtnngnccn	180
gcnwsnmgna aywsnggnyt ntayaayath acnttyaart aygayaaytg yacnacntay	240

ytnaayccng	tnggnaarca	ygtnathgcn	gaygcncara	ayathacnat	hwsncartay	300
gcntgycayg	aycargtngc	ngtnacnath	ytntggwsnc	cnggngcnyt	nggnathgar	360
ttyytnaarg	gnttymngt	nathytngar	garytnaarw	sngarggnmg	ncartgygar	420
carytnathy	tnaargaycc	naarcarytn	aaywsnwsnt	tyaarmgnac	nggnatggar	480
wsncarcnt	tyytnaayat	gaarttygar	acngaytayt	tygtnaargt	ngtnccntty	540
ccnwsnatha	araaygarws	naaytaycay	ccnttyttyt	tymgnacnmg	ngcntgygay	600
ytnytnytn	arccngayaa	yytngcntgy	aarccnttyt	ggaarccnmg	naayytnaay	660
athwsncarc	ayggngwsnga	yatgcargtn	wsnttygayc	aygcncncna	yaayttyggg	720
ttymgnttyt	tytayytnc	ytayaarytn	aarcaygarg	gncnttyaa	rmgnaaracn	780
tgyaarcarg	arcaracnac	ngaracnacn	wsntgyytny	tncaraaygt	nwsnccnggn	840
gaytayatha	thgarytngt	ngaygayacn	aayacnacnm	gnaargtnat	gcaytaygcn	900
ytnaarccng	tncaysncc	ntgggcnngn	ccnathmgng	cngtngcnat	hacngtnccn	960
ytngtngtna	thwsngcntt	ygcnacnytn	ttyacngtna	tgtgymgnaa	raarcargar	1020
garaayatht	aywsncayyt	ngaygargar	wsnwsngarw	snwsnacnta	yacngcngcn	1080
ytncnmgng	armgnytnmg	nccnmgnccn	aargtnttyy	tntgytayws	nwsnaargay	1140
ggncaraayc	ayatgaaygt	ngtncartgy	ttygcntayt	tyytncarga	ytytgyggg	1200
tgygargtng	cnytngayyt	ntgggargay	ttywsnytn	gymngarggg	ncarmnggar	1260
tgggtnathc	araarathca	ygarwsncar	ttyathathg	tngtntgyws	naarggnatg	1320
aartayttyg	tngayaaraa	raaytayaar	cayaarggng	gnggnmgngg	nwsnggnaar	1380
ggngarytn	tyytngtngc	ngtnwsngcn	athgcngara	arytnmgna	rgcnaarcar	1440
wsnwsnwsng	cngcnytnws	naarttyath	gcngtntayt	tygaytayws	ntgygarggn	1500
gaygtncng	gnathytnga	yytnwsnacn	aartaymgny	tnatggayaa	yytnccncar	1560
ytntgywsnc	ayytncayws	nmngngaycay	ggnytnrcarg	arccnggnca	rcayacnmgn	1620
carggnwsnm	gnmgnaayta	yttymgnwsn	aarwsnggnm	gnwsnytna	ygtnngcnath	1680
tgyaayatgc	aycarttyat	hgaygargar	ccngaytggt	tygaraarca	rttygtncn	1740
ttycayccnc	cncnytnmg	ntaymgngar	ccngtnytn	araarttyga	ywsnggnytn	1800
gtnytnaayg	aygtnatgtg	yaarccnggn	ccngarwsng	ayttytggyt	naargtngar	1860
gcngcngtny	tnggngcnac	nggnccngcn	gaywsncarc	aygarwsnca	rcayggnggn	1920
ytngaycarg	ayggngargc	nmgnccngcn	ytngayggngw	sngcngcnyt	ncarccnytn	1980
ytncayacng	tnaargcngg	nwsnccnwsn	gayatgccnm	gngaywsngg	nathtaygay	2040
wsnwsngtnc	cnwsnwsnga	rytnwsnytn	ccnytnatgg	arggnytnws	nacngaycar	2100
acngaracnw	snwsnytnac	ngarwsngtn	wsnwsnwsnw	snggnytnng	ngargargar	2160
ccncngcny	tnccnwsnaa	rytnytnwsn	wsnggnwsnt	gyaargcnga	yytnggntgy	2220
mgnwsntaya	cngaygaryt	ncaygcngtn	gcncnytn			2259

<210> 4

<211> 2383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)...(2344)

&lt;400&gt; 4

ccgccgcggc caccgcccac tcggggctgg ccagcggcgg gcggccgggg cgcagagaac	60
ggcctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc	112
Met Ala Pro Trp Leu Gln Leu Cys Ser	
1 5	
gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg	160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val	
10 15 20 25	
gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg	208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp	
30 35 40	
agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga	256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly	
45 50 55	
gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa	304
Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys	
60 65 70	
tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att	352
Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile	
75 80 85	
gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa	400
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln	
90 95 100 105	
gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc	448
Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe	
110 115 120	
ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga	496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg	
125 130 135	
cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc	544
Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	
140 145 150	

ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe 155 160 165	592
gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn 170 175 180 185	640
gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu 190 195 200	688
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg 205 210 215	736
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp 220 225 230	784
cac gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys 235 240 245	832
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln 250 255 260 265	880
act aca gag atg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp 270 275 280	928
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met 285 290 295	976
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg 300 305 310	1024
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr 315 320 325	1072

ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca	1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser	
330 335 340 345	
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc	1168
His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu	
350 355 360	
cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc	1216
Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser	
365 370 375	
agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac	1264
Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr	
380 385 390	
ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa	1312
Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu	
395 400 405	
gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag	1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys	
410 415 420 425	
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag	1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys	
430 435 440	
tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc	1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly	
445 450 455	
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa	1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu	
460 465 470	
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt	1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe	
475 480 485	
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc	1600

Ile	Ala	Val	Tyr	Phe	Asp	Tyr	Ser	Cys	Glu	Gly	Asp	Val	Pro	Gly	Ile	
490					495					500					505	
cta	gac	ctg	agt	acc	aag	tac	aga	ctc	atg	gac	aat	ctt	cct	cag	ctc	1648
Leu	Asp	Leu	Ser	Thr	Lys	Tyr	Arg	Leu	Met	Asp	Asn	Leu	Pro	Gln	Leu	
				510					515					520		
tgt	tcc	cac	ctg	cac	tcc	cga	gac	cac	ggc	ctc	cag	gag	ccg	ggg	cag	1696
Cys	Ser	His	Leu	His	Ser	Arg	Asp	His	Gly	Leu	Gln	Glu	Pro	Gly	Gln	
			525					530					535			
cac	acg	cga	cag	ggc	agc	aga	agg	aac	tac	ttc	cgg	agc	aag	tca	ggc	1744
His	Thr	Arg	Gln	Gly	Ser	Arg	Arg	Asn	Tyr	Phe	Arg	Ser	Lys	Ser	Gly	
		540					545					550				
cgg	tcc	cta	tac	gtc	gcc	att	tgc	aac	atg	cac	cag	ttt	att	gac	gag	1792
Arg	Ser	Leu	Tyr	Val	Ala	Ile	Cys	Asn	Met	His	Gln	Phe	Ile	Asp	Glu	
	555					560					565					
gag	ccc	gac	tgg	ttc	gaa	aag	cag	ttc	gtt	ccc	ttc	cat	cct	cct	cca	1840
Glu	Pro	Asp	Trp	Phe	Glu	Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	
570					575					580					585	
ctg	cgc	tac	cgg	gag	cca	gtc	ttg	gag	aaa	ttt	gat	tcg	ggc	ttg	gtt	1888
Leu	Arg	Tyr	Arg	Glu	Pro	Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	
				590					595					600		
tta	aat	gat	gtc	atg	tgc	aaa	cca	ggg	cct	gag	agt	gac	ttc	tgc	cta	1936
Leu	Asn	Asp	Val	Met	Cys	Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	
			605					610					615			
aag	gta	gag	gcg	gct	gtt	ctt	ggg	gca	acc	gga	cca	gcc	gac	tcc	cag	1984
Lys	Val	Glu	Ala	Ala	Val	Leu	Gly	Ala	Thr	Gly	Pro	Ala	Asp	Ser	Gln	
		620					625					630				
cac	gag	agt	cag	cat	ggg	ggc	ctg	gac	caa	gac	ggg	gag	gcc	cgg	cct	2032
His	Glu	Ser	Gln	His	Gly	Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro	
	635					640					645					
gcc	ctt	gac	ggt	agc	gcc	gcc	ctg	caa	ccc	ctg	ctg	cac	acg	gtg	aaa	2080
Ala	Leu	Asp	Gly	Ser	Ala	Ala	Leu	Gln	Pro	Leu	Leu	His	Thr	Val	Lys	
650					655					660					665	

gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg 2128  
Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser  
670 675 680

tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg 2176  
Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser  
685 690 695

acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct 2224  
Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser  
700 705 710

tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc 2272  
Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu  
715 720 725

tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat 2320  
Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp  
730 735 740 745

gaa ctc cac gcg gcc gcc cct ttg taacaaaacg aaagagtcta agcattgcc 2374  
Glu Leu His Ala Ala Ala Pro Leu  
750

cttttagctg 2383

<210> 5

<211> 753

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala  
1 5 10 15  
Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg  
20 25 30  
Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg  
35 40 45  
Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn  
50 55 60  
Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr  
65 70 75 80

Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr  
                     85                    90                    95  
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp  
                     100                    105                    110  
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile  
                     115                    120                    125  
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu  
                     130                    135                    140  
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu  
 145                    150                    155                    160  
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys  
                     165                    170                    175  
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe  
                     180                    185                    190  
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu  
                     195                    200                    205  
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His  
                     210                    215                    220  
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly  
 225                    230                    235                    240  
 Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe  
                     245                    250                    255  
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys  
                     260                    265                    270  
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp  
                     275                    280                    285  
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val  
                     290                    295                    300  
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro  
 305                    310                    315                    320  
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg  
                     325                    330                    335  
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser  
                     340                    345                    350  
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro  
                     355                    360                    365  
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His  
                     370                    375                    380  
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly  
 385                    390                    395                    400  
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu  
                     405                    410                    415

Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile  
 420 425 430  
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn  
 435 440 445  
 Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe  
 450 455 460  
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln  
 465 470 475 480  
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr  
 485 490 495  
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr  
 500 505 510  
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg  
 515 520 525  
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg  
 530 535 540  
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile  
 545 550 555 560  
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys  
 565 570 575  
 Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val  
 580 585 590  
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys  
 595 600 605  
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu  
 610 615 620  
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly  
 625 630 635 640  
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala  
 645 650 655  
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met  
 660 665 670  
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu  
 675 680 685  
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser  
 690 695 700  
 Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu  
 705 710 715 720  
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala  
 725 730 735  
 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Ala Ala Pro  
 740 745 750

Leu

&lt;210&gt; 6

&lt;211&gt; 2259

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2259)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 6

atggcncnt	ggytncaryt	ntgywsngtn	ttyttyacng	tnaaygcntg	yytnaayggn	60
wsncarytng	cngtngcngc	ngnggnwnsn	ggnmgngcnm	gngngcnga	yacntgyggn	120
tgmgnatga	argcngcngc	nmgnccnmgn	ytntgygtng	cnaaygargg	ngtnggnccn	180
gcnwsnmgna	aywsnggnyt	ntayaayath	acnttyaart	aygayaaytg	yacnacntay	240
ytnaayccng	tnggnaarca	ygtnathgcn	gaygcncara	ayathacnat	hwsncartay	300
gcntgycayg	aycargtngc	ngtnacnath	ytntggwsnc	cnggngcnyt	nggnathgar	360
ttyytnaarg	gnttymngt	nathytngar	garytnaarw	sngarggnmg	ncartgycar	420
carytnathy	tnaargaycc	naarcarytn	aaywsnwsnt	tyaarmgnac	nggnatggar	480
wsncarcnt	tyytnaayat	gaarttygar	acngaytayt	tygtnaargt	ngtnccntty	540
ccnwsnatha	araaygarws	naaytaycay	ccnttytyt	tymgnacnmg	ngcntgygay	600
ytntytytnc	arccngayaa	yytngcntgy	aarccnttyt	ggaarccnmg	naayytnaay	660
athwsncarc	ayggwnsnga	yatgcargtn	wsnttygayc	aygcncncna	yaayttyggn	720
ttymgnttyt	tytayytnc	ytayaarytn	aarcaygarg	gncnttyaa	rmgnaaracn	780
tgyaarcarg	arcaracnac	ngaratgacn	wsntgyytny	tncaraaygt	nwsnccnggn	840
gaytayatha	thgarytngt	ngaygayacn	aayacnacnm	gnaargtnat	gcaytaygcn	900
ytnaarccng	tncaysncc	ntgggcnggn	ccnathmgng	cngtngcnat	hacngtnccn	960
ytngtngtna	thwsngcntt	ygcnacnytn	ttyacngtna	tgtgymgnaa	raarcarc	1020
garaayatht	aywsncayyt	ngaygargar	wsnwsngarw	snwsnacnta	yacngcngcn	1080
ytncnmngng	armgnytnmg	nccnmgnccn	aargtnttyy	tntgytayws	nwsnaargay	1140
ggncaraayc	ayatgaaygt	ngtncartgy	ttygcntayt	tyytncarga	ytttygyggn	1200
tgygargtng	cnytngayyt	ntgggargay	ttywsnytn	gymngargg	ncarmngar	1260
tgggtathc	araarathca	ygarwsncar	ttyathathg	tngtntgyws	naarggnatg	1320
aartaytytg	tngayaaraa	raaytayaar	cayaarggng	gnggnmgngg	nwsnggnaar	1380
ggngarytn	tyytngtngc	ngtnwsngcn	athgcngara	arytnmgna	rgcnaarcar	1440
wsnwsnwsng	cngcnytnws	naarttyath	gcngtntayt	tygaytayws	ntgygarggn	1500
gaygtncng	gnathytnga	yytnwsnacn	aartaymgny	tnatggayaa	yytnccncar	1560
ytntgywsnc	ayytncayws	nmngngaycay	ggnytncarg	arccnggnca	rcayacnmgn	1620

```

carggnwsnm gnmgnaayta yttymgnwsn aarwsnggnm gnwsnytna ygtngcnath 1680
tgyaayatgc aycarttyat hgaygargar ccngaytggt tygaraarca rtytgtnccn 1740
ttycayccnc cncnytnmg ntaymgngar ccngtnytng araarttyga ywsnggnytn 1800
gtnytnaayg aygtnatgtg yaarccnggn ccngarwsng ayttytggyt naargtngar 1860
gcngcngtny tngngcnac nggncngcn gaywsncarc aygarwsnca rcayggnggn 1920
ytngaycarg ayggngargc nmgnccngcn ytngayggnw sngcngcnyt ncarccnytn 1980
ytncayacng tnaargcngg nwsnccnwsn gayatgccnm gngaywsngg nathtaygay 2040
wsnwsngtnc cnwsnwsnga rytwnsnytn ccnytnatgg arggnytnws nacngaycar 2100
acngaracnw snwsnytnac ngarwsngtn wsnwsnwsnw snggnytnng ngargargar 2160
ccncngcny tnccnwsnaa rytnytnwsn wsnggnwsnt gyaargcnga yytnggntgy 2220
mgnwsntaya cngaygaryt ncaygcngcn gcncnytn 2259

```

&lt;210&gt; 7

&lt;211&gt; 2341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (86)...(2302)

&lt;400&gt; 7

```

ccgccgcggc caccgcccac tcggggctgg ccagcggcgg gcggccgggg cgagagaaac 60
ggcctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc 112

```

Met Ala Pro Trp Leu Gln Leu Cys Ser

1

5

```

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg 160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
10 15 20 25

```

```

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg 208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
30 35 40

```

```

agg gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc 256
Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
45 50 55

```

```

ttc aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat 304
Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
60 65 70

```

gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His 75 80 85	352
gac caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile 90 95 100 105	400
gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu 110 115 120	448
gga aga cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn 125 130 135	496
agt agc ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met 140 145 150	544
aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile 155 160 165	592
aaa aac gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys 170 175 180 185	640
gac ctg ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys 190 195 200	688
cct cgg aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser 205 210 215	736
ttc gac cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His 220 225 230	784
tac aag ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln 235 240 245	832

gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca	880
Glu Gln Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro	
250 255 260 265	
ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa	928
Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys	
270 275 280	
gtg atg cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc	976
Val Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro	
285 290 295	
atc aga gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc	1024
Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe	
300 305 310	
gcg acg ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata	1072
Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile	
315 320 325	
tat tca cat tta gat gaa gag agc tct gag tct tcc aca tac act gca	1120
Tyr Ser His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala	
330 335 340 345	
gca ctc cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc	1168
Ala Leu Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys	
350 355 360	
tat tcc agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc	1216
Tyr Ser Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe	
365 370 375	
gcc tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg	1264
Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu	
380 385 390	
tgg gaa gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc	1312
Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile	
395 400 405	
cag aag atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt	1360

Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly	
410 415 420 425	
atg aag tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc	1408
Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly	
430 435 440	
cga ggc tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att	1456
Arg Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile	
445 450 455	
gcc gaa aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc	1504
Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser	
460 465 470	
aag ttt atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc	1552
Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro	
475 480 485	
ggt atc cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct	1600
Gly Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro	
490 495 500 505	
cag ctc tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg	1648
Gln Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro	
510 515 520	
ggg cag cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag	1696
Gly Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys	
525 530 535	
tca ggc cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att	1744
Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile	
540 545 550	
gac gag gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct	1792
Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro	
555 560 565	
cct cca ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc	1840
Pro Pro Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly	
570 575 580 585	

ttg gtt tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc	1888
Leu Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe	
590 595 600	
tgc cta aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac	1936
Cys Leu Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp	
605 610 615	
tcc cag cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc	1984
Ser Gln His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala	
620 625 630	
cgg cct gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg	2032
Arg Pro Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr	
635 640 645	
gtg aaa gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat	2080
Val Lys Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr	
650 655 660 665	
gac tcg tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga	2128
Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly	
670 675 680	
ctc tcg acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc	2176
Leu Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser	
685 690 695	
tcc tct tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag	2224
Ser Ser Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys	
700 705 710	
ctc ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac	2272
Leu Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr	
715 720 725	
act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta	2322
Thr Asp Glu Leu His Ala Val Ala Pro Leu	
730 735	
agcattgccca ctttagctg	2341

<210> 8  
 <211> 739  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met	Ala	Pro	Trp	Leu	Gln	Leu	Cys	Ser	Val	Phe	Phe	Thr	Val	Asn	Ala
1				5					10					15	
Cys	Leu	Asn	Gly	Ser	Gln	Leu	Ala	Val	Ala	Ala	Gly	Gly	Ser	Gly	Arg
			20					25					30		
Ala	Arg	Gly	Ala	Asp	Thr	Cys	Gly	Trp	Arg	Gly	Val	Gly	Pro	Ala	Ser
			35				40					45			
Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	Lys	Tyr	Asp	Asn	Cys	Thr
	50					55					60				
Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala	Gln	Asn
65					70				75					80	
Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile
				85					90					95	
Leu	Trp	Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly	Phe	Arg
			100					105					110		
Val	Ile	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Cys	Gln	Gln	Leu
		115					120					125			
Ile	Leu	Lys	Asp	Pro	Lys	Gln	Leu	Asn	Ser	Ser	Phe	Lys	Arg	Thr	Gly
	130					135					140				
Met	Glu	Ser	Gln	Pro	Phe	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe
145					150					155				160	
Val	Lys	Val	Val	Pro	Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His
				165					170					175	
Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	Asp
			180					185					190		
Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser
	195						200					205			
Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	Asn
	210					215				220					
Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	Gly
225					230					235				240	
Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Thr	Thr
				245					250				255		
Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	Leu
		260						265					270		
Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	Lys
	275						280						285		

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr  
 290 295 300  
 Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met  
 305 310 315 320  
 Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu  
 325 330 335  
 Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu  
 340 345 350  
 Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln  
 355 360 365  
 Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe  
 370 375 380  
 Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys  
 385 390 395 400  
 Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln  
 405 410 415  
 Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys  
 420 425 430  
 Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu  
 435 440 445  
 Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala  
 450 455 460  
 Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe  
 465 470 475 480  
 Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr  
 485 490 495  
 Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His  
 500 505 510  
 Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly  
 515 520 525  
 Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val  
 530 535 540  
 Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe  
 545 550 555 560  
 Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu  
 565 570 575  
 Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met  
 580 585 590  
 Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala  
 595 600 605  
 Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His  
 610 615 620

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser  
 625 630 635 640  
 Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser  
 645 650 655  
 Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser  
 660 665 670  
 Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu  
 675 680 685  
 Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu  
 690 695 700  
 Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys  
 705 710 715 720  
 Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val  
 725 730 735  
 Ala Pro Leu

<210> 9

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc\_feature

<222> (1)...(2217)

<223> n = A,T,C or G

<400> 9

atggcncnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaaygg	60
wsncarytng cngtngcngc ngnggnwnsn ggnmgngcnm gnggngcnga yacntgygg	120
tggmgnggng tnggncngc nwsnmgnaay wsnggnytn tayaayathac nttyaartay	180
gayaaytgya cnactayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay	240
athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn	300
gngcnytn gnatggartt yytnaarggn ttymngntna thytnagara rytnaarwsn	360
garggnmgnc artgyarca rytnathytn aargayccna arcarytnaa ywsnwsntty	420
aarmgnacng gnatggarws ncarcntty ytnaayatga arttygarac ngaytayty	480
gtnaargtn tncnttycc nwsnathaar aaygarwsna aytaycaycc nttyttyty	540
mgnacnmng cntgygayyt nytnytn car cngayaay tngcntgyaa rcnttytg	600
aarcnmgna ayytnaayat hwsncarcay ggnwsngaya tgcargtnws nttygaycay	660
gcncncaya aytyggntt ymgnttytty tayytncayt ayaarytnaa rcaygarggn	720
ccnttyaarm gnaaracntg yaarcargar caracnacng aracnacnws ntgyytnytn	780

caraaygtnw	sncngnga	ytayathath	garytngtng	aygayacnaa	yacnacnmgn	840
aargtnatgc	aytaygcnyt	naarccngtn	caywsnccnt	ggcnggncc	nathmgngcn	900
gtngcnatha	cngtnccnyt	ngtngtnath	wsngcnttyg	cnacnytnnt	yacngtnatg	960
tgymgnaara	arcarcarga	raayathtay	wsncayytng	aygargarws	nwsngarwsn	1020
wsnacntaya	cngcngcnyt	nccnmngnar	mgnytnmgnc	cnmgncnaa	rgtnnttytn	1080
tgytaywsnw	snaargaygg	ncaraaycay	atgaaygtng	tncartgytt	ygcntaytty	1140
ytnccargayt	tytggygntg	ygargtngcn	ytngayytnt	gggargaytt	ywsnytnngy	1200
mgngarggnc	armgngartg	ggtnathcar	aarathcayg	arwsncartt	yathathgtt	1260
gtntgywsna	arggnatgaa	rtayttygtt	gayaaraara	aytayaarca	yaarggnggn	1320
ggnmngngnw	snggnaargg	ngarytnntt	ytngtngcng	tnwsngcnat	hgcnagaraar	1380
ytnmgncarg	cnaarcarws	nwsnwsngcn	gcnytnwsna	arttyathgc	ngtntaytty	1440
gaytaywsnt	gygarggnga	ygtnccnggn	athytnngay	tnwsnacnaa	rtaymgnytn	1500
atggayaayy	tnccncaryt	ntgywsncay	ytnccaywsnm	gngaycaygg	nytnccargar	1560
ccnggncarc	ayacnmgnca	rggnwsnmgn	mgnaaytayt	tymgnwsnaa	rwsnggnmg	1620
wsnytnatyg	tngcnathtg	yaayatgcay	carttyathg	aygargarcc	ngaytggtty	1680
garaarcart	tygtncntt	ycayccncn	ccnytnmgnt	aymgngarcc	ngtnytnngar	1740
aarttygayw	snggnytngt	nytnaaygay	gtatgtgya	arccnggncc	ngarwsngay	1800
ttytgyytna	argtnargc	ngcngtnytn	ggngcnacng	gnccngcnga	ywsncarcay	1860
garwsncarc	ayggnggnyt	ngaycargay	ggngargcnm	gnccngcnyt	ngayggnwsn	1920
gcngcnytn	arccnytnyt	ncayacngtn	aargcnggnw	sncnwsnga	yatgccnmgn	1980
gaywsnggna	thtaygayws	nwsngtnccn	wsnwsngary	tnwsnytncc	nytnatggar	2040
ggnytnwsna	cngaycarac	ngaracnwsn	wsnytnacng	arwsngtnws	nwsnwsnwsn	2100
ggnytnngng	argargarcc	nccngcnytn	ccnwsnaary	tnytnwsnws	nggnwsntgy	2160
aargcngayy	tnggntgymg	nwsntayacn	gaygarytn	aygngtngc	nccnytn	2217

<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 10

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 11

<211> 2443

<212> DNA

<213> Mouse

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)...(2317)

&lt;400&gt; 11

ctcggccgcc gccgctacca ccgccgccca ctcgggacta gagagcgagc tacaggcagc	60
aacctagcgg agaccggccc aactgggcga gcgtacggcc atg gcc ccg tgg ctg	115
Met Ala Pro Trp Leu	
1 5	
cag ctc tgc tcc ttc ttc ttc act gtc aac gcc tgt ctc aac ggc tgc	163
Gln Leu Cys Ser Phe Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser	
10 15 20	
cag ctg gca gtg gcc gcg ggc ggc tcc ggc cgc gcg agg ggc gcg gac	211
Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp	
25 30 35	
acc tgt ggc tgg agg gga gtg ggg ccg gcc agc agg aac agc gga ctg	259
Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu	
40 45 50	
cac aac atc acc ttc aga tac gac aac tgt acc acc tac ttg aat ccc	307
His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro	
55 60 65	
ggc ggc ggc aag cat gcg att gct gat gct cag aac atc acc atc agc	355
Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser	
70 75 80 85	
cag tac gct tgc cac gac cag gtg gca gtc acc att ctt tgg tcc cca	403
Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro	
90 95 100	
ggg gcc ctt ggc att gaa ttc cta aaa gga ttc cga gtc atc ctg gag	451
Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu	
105 110 115	
gag ctg aag tcg gag ggc aga cag tgc caa cag ctg att cta aag gac	499
Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp	
120 125 130	
ccc aaa cag ctc aac agc agc ttc aga agg act gga atg gaa tct cag	547

Pro	Lys	Gln	Leu	Asn	Ser	Ser	Phe	Arg	Arg	Thr	Gly	Met	Glu	Ser	Gln		
135						140					145						
cct	ttc	ctg	aat	atg	aaa	ttt	gag	acg	gat	tac	ttt	gta	aag	att	gtc	595	
Pro	Phe	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe	Val	Lys	Ile	Val		
150					155				160					165			
cct	ttc	cct	tcc	att	aaa	aat	gaa	agc	aat	tac	cat	ccc	ttc	ttc	ttc	643	
Pro	Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His	Pro	Phe	Phe	Phe		
				170					175					180			
aga	aca	cgg	gcc	tgt	gac	ctg	ttg	tta	caa	cct	gac	aac	ttg	gcc	tgt	691	
Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Gln	Pro	Asp	Asn	Leu	Ala	Cys			
			185					190					195				
aag	cct	ttc	tgg	aag	cct	cga	aac	ctg	aat	atc	agc	cag	cat	ggg	tct	739	
Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser	Gln	His	Gly	Ser		
		200					205					210					
gac	atg	cac	gtg	tcc	ttc	gac	cat	gcc	ccg	cag	aac	ttc	ggc	ttc	cgt	787	
Asp	Met	His	Val	Ser	Phe	Asp	His	Ala	Pro	Gln	Asn	Phe	Gly	Phe	Arg		
	215					220					225						
ggc	ttc	cat	gtt	ctc	tat	aag	ctc	aag	cac	gaa	ggc	ccc	ttc	agg	cgg	835	
Gly	Phe	His	Val	Leu	Tyr	Lys	Leu	Lys	His	Glu	Gly	Pro	Phe	Arg	Arg		
230				235						240				245			
agg	act	tgc	agg	cag	gac	cag	aat	aca	gag	aca	acc	agc	tgc	ctc	ctc	883	
Arg	Thr	Cys	Arg	Gln	Asp	Gln	Asn	Thr	Glu	Thr	Thr	Ser	Cys	Leu	Leu		
				250					255					260			
caa	aac	gtt	tct	cca	ggg	gac	tat	atc	att	gag	ctg	gtg	gat	gac	agc	931	
Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	Leu	Val	Asp	Asp	Ser		
		265					270						275				
aac	acc	acc	agg	aaa	gct	gct	cag	tat	gtg	gtg	aag	tca	gtg	cag	tct	979	
Asn	Thr	Thr	Arg	Lys	Ala	Ala	Gln	Tyr	Val	Val	Lys	Ser	Val	Gln	Ser		
		280					285					290					
ccc	tgg	gct	gga	ccc	atc	aga	gct	gtg	gcc	atc	act	gtg	cct	ctg	gtt	1027	
Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile	Thr	Val	Pro	Leu	Val		
295						300					305						

gtc ata tct gcg ttc gca acc ctg ttc act gtg atg tgc aga aag aag	1075
Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys	
310 315 320 325	
caa caa gaa aat ata tat tca cat tta gat gaa gaa agc ccg gag tcg	1123
Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser	
330 335 340	
tcc aca tac gct gcg gct ctc ccc aga gac agg ctc cgg cct cag ccc	1171
Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg Leu Arg Pro Gln Pro	
345 350 355	
aag gtc ttc ctc tgc tac tcc aat aaa gat ggc cag aat cac atg aac	1219
Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly Gln Asn His Met Asn	
360 365 370	
gtg gtc cag tgt ttc gcc tat ttc ctg caa gat ttc tgt ggc tgt gag	1267
Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu	
375 380 385	
gtg gct ctg gac ttg tgg gaa gat ttc agc ctc tgc aga gag ggg cag	1315
Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln	
390 395 400 405	
aga gaa tgg gcc att cag aag atc cac gag tcc cag ttc atc att gtc	1363
Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val	
410 415 420	
gtg tgc tcc aaa ggc atg aag tac ttt gta gat aag aag aac ttc aga	1411
Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Phe Arg	
425 430 435	
cac aaa gga ggc agc cgc ggc gag gcg caa ggc gag ttc ttc ctg gtg	1459
His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly Glu Phe Phe Leu Val	
440 445 450	
gcc gtg gca gcc att gct gag aag ctc cgt cag gcc aag cag agc tca	1507
Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser	
455 460 465	
tct gcc gca ctg cgc aag ttc atc gcc gtc tac ttc gat tat tcc tgt	1555

Ser	Ala	Ala	Leu	Arg	Lys	Phe	Ile	Ala	Val	Tyr	Phe	Asp	Tyr	Ser	Cys	
470					475					480					485	
gaa ggg gat gta ccc tgc agc ctg gac ctg agc acc aag tac aag ctc																1603
Glu	Gly	Asp	Val	Pro	Cys	Ser	Leu	Asp	Leu	Ser	Thr	Lys	Tyr	Lys	Leu	
			490						495					500		
atg gac cac ctt cct gag ctc tgt gcc cat ctg cac tca gga gag cag																1651
Met	Asp	His	Leu	Pro	Glu	Leu	Cys	Ala	His	Leu	His	Ser	Gly	Glu	Gln	
			505					510					515			
gag gtg ctg ggt cag cac cca ggc cac agc agc aga agg aac tac ttc																1699
Glu	Val	Leu	Gly	Gln	His	Pro	Gly	His	Ser	Ser	Arg	Arg	Asn	Tyr	Phe	
		520					525					530				
cgg agc aaa tcg ggc cgc tcc ctg tat gtt gcc att tgc aac atg cac																1747
Arg	Ser	Lys	Ser	Gly	Arg	Ser	Leu	Tyr	Val	Ala	Ile	Cys	Asn	Met	His	
	535					540				545						
cag ttt att gat gag gag cct gac tgg ttt gag aag cag ttt ata ccc																1795
Gln	Phe	Ile	Asp	Glu	Glu	Pro	Asp	Trp	Phe	Glu	Lys	Gln	Phe	Ile	Pro	
550					555					560					565	
ttc caa cat ccc cct gtg cgc tac cag gag cca gtc ctg gag aaa ttt																1843
Phe	Gln	His	Pro	Pro	Val	Arg	Tyr	Gln	Glu	Pro	Val	Leu	Glu	Lys	Phe	
			570					575					580			
gac tca ggc ttg gtt tta aat gat gtc ata agc aaa cca ggg cca gag																1891
Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val	Ile	Ser	Lys	Pro	Gly	Pro	Glu	
			585					590					595			
agt gac ttc tgt cgg aaa gtc gag gct tgt gta ctt ggg gcc gct ggg																1939
Ser	Asp	Phe	Cys	Arg	Lys	Val	Glu	Ala	Cys	Val	Leu	Gly	Ala	Ala	Gly	
	600						605				610					
cca gcc gac tct tat tca tac ctg gag agt cag cat gta ggc ctg gac																1987
Pro	Ala	Asp	Ser	Tyr	Ser	Tyr	Leu	Glu	Ser	Gln	His	Val	Gly	Leu	Asp	
	615					620				625						
caa gac act gag gcc cag ccc tcc tgt gat agt gcc cct gcc ttg cag																2035
Gln	Asp	Thr	Glu	Ala	Gln	Pro	Ser	Cys	Asp	Ser	Ala	Pro	Ala	Leu	Gln	
630					635					640					645	

ccc ctg tta cac gca gtg aaa gct ggc agt ccc tca gag atg cca cgg 2083  
 Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro Ser Glu Met Pro Arg  
 650 655 660

gac tca ggc ata tat gat tct tct gta ccc tca tca gag ctc tct ctg 2131  
 Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu  
 665 670 675

cct ctg atg gag gga ctc tcc ccg gat cag ata gaa aca tct tct ctg 2179  
 Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile Glu Thr Ser Ser Leu  
 680 685 690

acc gag agt gta tct tcc tcc tct ggc cta ggt gag gag gac ccc cct 2227  
 Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Asp Pro Pro  
 695 700 705

acc ctc cct tcc aag ctc ttt gcc tct ggg gtg tcc aga gaa cat ggt 2275  
 Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val Ser Arg Glu His Gly  
 710 715 720 725

tgc cac agc cac act gac gaa ctg caa gcg ctt gct cct ttg 2317  
 Cys His Ser His Thr Asp Glu Leu Gln Ala Leu Ala Pro Leu  
 730 735

taaggactcg gaagagtcta agcatcgcca cttagctgc tgatctctct ggctccccag 2377  
 ttcacctctg tggttgtgca gcctacttgg agctgaaggc gcacacgggg atatctggaa 2437  
 tgaaat 2443

&lt;210&gt; 12

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 12

Met Ala Pro Trp Leu Gln Leu Cys Ser Phe Phe Phe Thr Val Asn Ala  
 1 5 10 15  
 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg  
 20 25 30  
 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser  
 35 40 45  
 Arg Asn Ser Gly Leu His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr  
 50 55 60

Thr Tyr Leu Asn Pro Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln  
 65 70 75 80  
 Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr  
 85 90 95  
 Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe  
 100 105 110  
 Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln  
 115 120 125  
 Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr  
 130 135 140  
 Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr  
 145 150 155 160  
 Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr  
 165 170 175  
 His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro  
 180 185 190  
 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile  
 195 200 205  
 Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln  
 210 215 220  
 Asn Phe Gly Phe Arg Gly Phe His Val Leu Tyr Lys Leu Lys His Glu  
 225 230 235 240  
 Gly Pro Phe Arg Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr  
 245 250 255  
 Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu  
 260 265 270  
 Leu Val Asp Asp Ser Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val  
 275 280 285  
 Lys Ser Val Gln Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile  
 290 295 300  
 Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val  
 305 310 315 320  
 Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu  
 325 330 335  
 Glu Ser Pro Glu Ser Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg  
 340 345 350  
 Leu Arg Pro Gln Pro Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly  
 355 360 365  
 Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp  
 370 375 380  
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu  
 385 390 395 400

Cys Arg Glu Gly Gln Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser  
 405 410 415  
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp  
 420 425 430  
 Lys Lys Asn Phe Arg His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly  
 435 440 445  
 Glu Phe Phe Leu Val Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln  
 450 455 460  
 Ala Lys Gln Ser Ser Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr  
 465 470 475 480  
 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser  
 485 490 495  
 Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu  
 500 505 510  
 His Ser Gly Glu Gln Glu Val Leu Gly Gln His Pro Gly His Ser Ser  
 515 520 525  
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala  
 530 535 540  
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu  
 545 550 555 560  
 Lys Gln Phe Ile Pro Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro  
 565 570 575  
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser  
 580 585 590  
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val  
 595 600 605  
 Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln  
 610 615 620  
 His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser  
 625 630 635 640  
 Ala Pro Ala Leu Gln Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro  
 645 650 655  
 Ser Glu Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser  
 660 665 670  
 Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile  
 675 680 685  
 Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly  
 690 695 700  
 Glu Glu Asp Pro Pro Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val  
 705 710 715 720  
 Ser Arg Glu His Gly Cys His Ser His Thr Asp Glu Leu Gln Ala Leu  
 725 730 735

Ala Pro Leu

&lt;210&gt; 13

&lt;211&gt; 2217

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> This degenerate nucleotide sequence encodes the  
amino acid sequence of SEQ ID NO:12.

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2217)

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 13

atggcncnt	ggytncaryt	ntgywsntty	ttyttyacng	tnaaygcntg	yytnaayggn	60
wsncarytng	cngtngcngc	nggnggnwsn	gngmngncnm	gnggngcnga	yacntgyggn	120
tggmngggng	tnggnccngc	nwsnmgnaay	wsnggnytn	ayaayathac	nttymgntay	180
gayaaytgga	cnacntayyt	naayccnggn	ggnggnaarc	aygcnathgc	ngaygcncar	240
aayathacna	thwsncarta	ygcntgygay	gaycargtng	cngtnacnat	hytntggwsn	300
ccnggngcny	tnggnathga	rttyytnaar	ggnttymgng	tnathytnga	rgarytnaar	360
wsngarggng	gncartgyca	rcarytnath	ytnaargayc	cnaarcaryt	naaywsnwsn	420
ttygmngmna	cnggnatgga	rwsncarccn	ttyytnaaya	tgaarttyga	racngaytay	480
ttygtnaara	thgtncntt	yccnwsnath	aaraaygarw	snaaytayca	yccnttytty	540
ttygmgnacnm	gngcntgyga	yytnytnytn	carccngaya	ayytngcntg	yaarcntty	600
tggaarccnm	gnaayytnaa	yathwsncar	cayggngwsng	ayatgcaygt	nwsnttygay	660
caygcncnc	araaytgyg	nttymnggn	ttycaygtny	tntayaaryt	naarcaygar	720
ggncnttym	gnmgnmgnac	ntgymgncar	gaycaraaya	cngaracnac	nwsntgyytn	780
ytncaraayg	tnwsnccngg	ngaytayath	athgarytng	tngaygayws	naayacnacn	840
mgnaargcng	cncartaygt	ngtnaarwsn	gtncarwsnc	cntgggcnng	nccnathmgn	900
gcngtngcna	thacngtncc	nytngtngtn	athwsngcnt	tygcnacny	nttyacngtn	960
atgtgymgna	araarcarca	rgaraayath	taywsncayy	tngaygarga	rwsnccngar	1020
wsnwsnacnt	aygcngcngc	nytnccnmgn	gaymgnytnm	gnccncarcc	naargtntty	1080
ytntgytayw	snaayaarga	yggncaraay	cayatgaayg	tngtncartg	ytytygcntay	1140
ttyytncarg	ayttytgygg	ntgygargtn	gcnytngayy	tntgggarga	ytytwsnytn	1200
tgymngarg	gncarmgnga	rtgggcnath	caraarathc	aygarwsnca	rttyathath	1260
gtngtntgyw	snaarggnat	gaartaytty	gtngayaara	araayttymg	ncayaarggn	1320
ggnwsnmng	gngargcnca	rgnggartty	ttyytngtng	cngtngcngc	nathgcngar	1380
aarytnmgnc	argcnaarca	rwsnwsnwsn	gcngcnytnm	gnaarttyat	hgcngtntay	1440
ttygaytayw	sntgygargg	ngaygtncn	tgywsnytn	ayytnwsnac	naartayaar	1500
ytnatggayc	ayytnccnga	rytntgygcn	cayytncayw	sngnggarca	rgargtnytn	1560
ggncarcayc	cnggncayws	nwsnmgnmgn	aaytayttym	gnwsnaarws	nggnmgnwsn	1620

